

AMENDMENTS TO THE SPECIFICATION

Substitute Table 3 on page 19 with the following:

Table 3. Listed are the 8 virulence genes and 16S rDNA used in the multiplex-PCR assay, together with amplicon size, final primer concentration, and primer sequences.

Virulence Factor	<i>E. coli</i> group	Gene locus	Primer-name	Amplicon size (bp)	Primer conc. (μM)	Primer sequence (5'→3')
Heat labile enterotoxin I (LT1)	ETEC	<i>elt</i>	LT-F	479	0.4	SEQ ID NO:1: AAACCGGCTTTG-TCAGATATGATG
			LT-R		0.4	nt 1 – 22 of SEQ ID NO:2: TGTGCTCAGAT-TCTGGGTCTCC
Heat stable enterotoxin I (ST1)	ETEC	<i>sta</i>	ST-F	171	0.25	SEQ ID NO:3: TCACCTTTTCG-CTCAGGATGC
			ST-R		0.25	SEQ ID NO:4: ATAGCACCCG-GTACAAGCAGG
		<i>estA-humane</i>	ST-Fh	151	0.4	SEQ ID NO:5: TTTCGCTCAGGA TGCTAAACCAG
			ST-Rh		0.4	SEQ ID NO:6: CAGGATTACAACA CAATTCACAGCAGTA
		<i>estA-porcine</i>	ST-Fp	160	0.4	SEQ ID NO:7: CTTTCCCTCTTTTAGTCAGTC AACTG
			ST-Rp		0.4	SEQ ID NO:8: CAGGATTACAACAAAGTTCAC AGCAG
Intimin (Eae)	EPEC /	<i>eae</i>	eae-F	377	0.2	SEQ ID NO:9: GGYCAGCGTT-TTTCCTTCCTG
	VTEC		eae-R		0.2	SEQ ID NO:11 TCGTCACCAR-AGGAATCGGAG
Shiga toxin 1 (Stx1) /	VTEC	<i>stx1</i> /	VT1-F	260	0.25	SEQ ID NO:13: GTTTGCAGTTG-ATGTCAGAGGGA
Verocytotoxin 1 (VT1)	<i>Shigella</i>	<i>vtx1</i>	VT1-R		0.25	SEQ ID NO:14: CAACGAATGG-CGATTTATCTGC
Shiga toxin 2 (Stx 2) /	VTEC	<i>stx2</i> /	VT2-F	420	0.25	SEQ ID NO:15: GGAATGCAAATC-AGTCGTCACCTC
Verocytotoxin 2 (VT2)		<i>vxt2</i>	VT2-R		0.25	SEQ ID NO:16: GCCTGTGCGCA-GTTATCTGACA
Invasion plasmid	EIEC /	<i>ipaH</i>	ipaH-F	647	0.1	SEQ ID NO:17: TTGACCGCT-TTCCGATACC

antigen H (ipaH)	<i>Shigella</i>		ipaH-R		0.1	SEQ ID NO:18: ATCCGCATCA- CCGCTCAGAC
Entero-hemolysin	VTEC /	<i>ehxA</i>	ehx-F	533	0.05	SEQ ID NO:19: GGGAAAAGCC- GGAACAGTTCT
A (EhxA)	EPEC		ehx-R		0.05	SEQ ID NO:20: CCAGCATAAC- AGCCGATGTGAT
bundle-forming	EPEC	<i>bfpA</i>	bfp-F	307	0.4	SEQ ID NO:21: TCCAATAAGKC- GCAGAATGCTA
pilus A (BfpA)			bfp-R		0.4	SEQ ID NO:23: CACCGTAGCCT- TTCGCTGAAG
16S rDNA	most	<i>16S</i>	16S-F	1062	0.25	SEQ ID NO:24: GGAGGCAGCA- GTGGGGAATA
	gram ÷		16S-R		0.25	SEQ ID NO:25: TGACGGGCGG- TGTGTACAAG

R = G or A, Y = C or T, K = G or T

Substitute Table 7, page 36, with the following:

Table 7. Oligonucleotide sequence of the capture probes used in the hybridization analyses of the 9 genes.

Probe design is described in "Detailed description of the invention".

Virulence factor	Encoded by gene	Oligonucleotide probe sequences (5'→3')
Heat labile entero-toxin I (LT)	<i>elt</i>	SEQ ID NO:26: CTGGATTCATCATGCACCACAAGGTTGTG
Heat stable entero-toxin I (ST)	<i>Sta</i>	SEQ ID NO:27: CACAGCAGTAATTGCTACTATTCATGCTTTCAGGA
Heat stable entero-toxin I (ST) human	<i>estA-human</i>	SEQ ID NO:28: GTCCTGAAAGCATGAATAGTAGCAA
Heat stable entero-toxin I (ST) porcine	<i>estA-porcine</i>	SEQ ID NO: 29: GAGACTAAAAAGTGTGATGTTGTAAA
Intimin (Eae)	<i>eae</i>	SEQ ID NO: 30: TACCCGTTTAGGTATTGGTGGCGAATACTGG
Verocytotoxin 1 (VT1)	<i>vtx1</i>	SEQ ID NO:31: TCCAGAGGAAGGGCGGTTTAATAATCTACGG
Verocytotoxin 2 (VT2)	<i>vtx2</i>	SEQ ID NO:32: TGGTTTCATCATATCTGGCGTTAATGGAGTTCAG
Invasion plasmid antigen H (IpaH)	<i>ipaH</i>	SEQ ID NO:33: CCAGCATCTCATACTTCTGCTCTTCTGCCTG
Enterohemolysin A (EhxA)	<i>ehxA</i>	SEQ ID NO:34: TGCTGAGAAAACAACGGGAAGGAGAGGA
Bundle-forming pilus A (BfpA)	<i>bfpA</i>	SEQ ID NO: 35: TCAGAAGTAATGAGCGCAACGTCTGCAATT
16S rDNA	<i>16S</i>	SEQ ID NO:36: AACGTATTCACCGTGGCATTCTGATCCAC